## CLAIMS

What is claimed is:

1. A composition comprising an isolated polynucleotide comprising a nucleotide sequence encoding a first polypeptide of at least 100 amino acids that has at least 85% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of a polypeptide of SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, 16, 18, and 20, or an isolated polynucleotide comprising the complement of the nucleotide sequence.

2. The composition of Claim 1, wherein the isolated nucleotide sequence consists of a nucleic acid sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, and 19 that codes for the polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, 16, 18, and 20.

3. The composition of Claim 1 wherein the isolated polynucleotide is DNA.

4. The composition of Claim 1 wherein the isolated polynucleotide is RNA.

5. A chimeric gene comprising the isolated polynucleotide of Claim 1 operably linked to suitable regulatory sequences.

6. An isolated host cell comprising the chimeric gene of Claim 5 or the isolated polynucleotide of Claim 1.

7. An isolated host cell comprising an isolated polynucleotide of Claim 1.

8. The isolated host cell of Claim 7 wherein the isolated host selected from the group consisting of yeast, bacteria, plant, and virus.

9. A virus comprising the isolated polynucleotide of Claim 1.

10. A composition comprising a polypeptide of at least 100 amino acids that has at least 85% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of a polypeptide of SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, 16, 18, and 20.

11. A method of selecting an isolated polynucleotide that affects the level of expression of a polypeptide in a plant cell, the method comprising the steps of:

constructing an isolated polynucleotide comprising a nucleotide sequence of at least one of 30 contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, and the complement of such nucleotide sequences;

introducing the isolated polynucleotide into a plant cell; and

measuring the level of a polypeptide in the plant cell containing the polynucleotide.

12. The method of Claim 11 wherein the isolated polynucleotide consists of a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, and 19 that codes for the polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, 16, 18, and 20.

13. A method of selecting an isolated polynucleotide that affects the level of expression of polypeptide in a plant cell, the method comprising the steps of:

constructing an isolated polynucleotide of Claim 1;

introducing the isolated polynucleotide into a plant cell; and

measuring the level of polypeptide in the plant cell containing the polynucleotide.

14. A method of obtaining a nucleic acid fragment encoding a polypeptide comprising the steps of:

synthesizing an oligonucleotide primer comprising a nucleotide sequence of at least one of 40 contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, and the complement of such nucleotide sequences; and

amplifying a nucleic acid sequence using the oligonucleotide primer.

15. A method of obtaining a nucleic acid fragment encoding the amino acid sequence encoding a protein disulfide isomerase polypeptide comprising the steps of:

probing a cDNA or genomic library with an isolated polynucleotide comprising a nucleotide sequence of at least one of 30 contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, and the complement of such nucleotide sequences; and

identifying a DNA clone that hybridizes with the isolated polynucleotide.

Add B8)

add C3)